

P. Ben

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form: DEC 14 2000

TECH CENTER 1600/2900

Application Serial Number: 09/284,697

Source: 1638

Date Processed by STIC: 12/1/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/284,697

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☒ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

P. BUI

#106
12/19/00
1638

IMPORTANT: see item 5 on
Erra summary sheet
Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/284,697

DATE: 12/01/2000
TIME: 08:23:23

Input Set : A:\ES.txt
Output Set: N:\CRF3\12012000\I284697.raw

3 <110> APPLICANT: MERTSTEM THERAPEUTICS S.A.
5 <120> TITLE OF INVENTION: Pancreatic Lipases and/or Recombinant Colipases and
6 Derived Polypeptides Produced by Plants, Methods for
7 Obtaining Them and UseThereof.

9 <130> FILE REFERENCE: 1074-1168PCT-US octobre 2000

11 <140> CURRENT APPLICATION NUMBER: US 09/284,697

12 <141> CURRENT FILING DATE: 1999-07-06

14 <150> PRIOR APPLICATION NUMBER: PCT/FR97/01862

15 <151> PRIOR FILING DATE: 1997-10-17

17 <160> NUMBER OF SEQ ID NOS: 16

19 <170> SOFTWARE: PatentIn Ver. 2.1

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 69

23 <212> TYPE: DNA

24 <213> ORGANISM: Artificial Sequence

26 <220> FEATURE:

27 <223> OTHER INFORMATION: Description of Artificial Sequence: signal peptide

29 <220> FEATURE:

30 <221> NAME/KEY: misc_feature

31 <222> LOCATION: (1)..(69)

32 <223> OTHER INFORMATION: Signal peptide of Sporamine A of Sweet potato

34 <220> FEATURE:

35 <221> NAME/KEY: CDS

36 <222> LOCATION: (1)..(69)

38 <300> PUBLICATION INFORMATION:

39 <303> JOURNAL: J. Biol. Chem.

40 <304> VOLUME: 264

41 <306> PAGES: 20042-20048

42 <307> DATE: 1989

44 <400> SEQUENCE: 1

45 atg aaa gcc ttc aca ctc gct ctc ttc tta gct ctt tcc ctc tat ctc 48

46 Met Lys Ala Phe Thr Leu Ala Leu Phe Leu Ala Leu Ser Leu Tyr Leu

47 1 5 10 15

49 ctg ccc aat cca gcc cat tcc 69

50 Leu Pro Asn Pro Ala His Ser

51 20

54 <210> SEQ ID NO: 2

55 <211> LENGTH: 23

56 <212> TYPE: PRT

57 <213> ORGANISM: Artificial Sequence

W--> 58 <220> FEATURE: Insert this mandatory numeric identifier whenever

58 <223> OTHER INFORMATION: Description of Artificial Sequence: signal peptide

60 <400> SEQUENCE: 2

61 Met Lys Ala Phe Thr Leu Ala Leu Phe Leu Ala Leu Ser Leu Tyr Leu

62 1 5 10 15

64 Leu Pro Asn Pro Ala His Ser

65 20

Sequence 1 is a nucleotide sequence.

It is would be a sufficient
Explanation for C2137 Artificial
Sequence.

↓
C2217, C2227, or
C2237 is
source
of genetic material

see circled portion of item 12
on Erra summary sheet

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/284,697

DATE: 12/01/2000
TIME: 08:23:23

Input Set : A:\ES.txt
Output Set: N:\CRF3\12012000\I284697.raw

69 <210> SEQ ID NO: 3
70 <211> LENGTH: 111
71 <212> TYPE: DNA
72 <213> ORGANISM: Artificial Sequence
74 <220> FEATURE:
75 <223> OTHER INFORMATION: Description of Artificial Sequence: Signal peptide
77 <220> FEATURE:
78 <221> NAME/KEY: sig_peptide
79 <222> LOCATION: (1)..(111)
80 <223> OTHER INFORMATION: Signal peptide PPS of Sporamine A of Sweet potato.
82 <220> FEATURE:
83 <221> NAME/KEY: CDS
84 <222> LOCATION: (1)..(111)
86 <300> PUBLICATION INFORMATION:
87 <303> JOURNAL: J. Biol. Chem.
88 <304> VOLUME: 264
89 <306> PAGES: 20042-20048
90 <307> DATE: 1989
92 <400> SEQUENCE: 3
93 atg aaa gcc ttc aca ctc gct ctc ttc tta gct ctt tcc ctc tat ctc 48
94 Met Lys Ala Phe Thr Leu Ala Leu Phe Leu Ala Leu Ser Leu Tyr Leu
95 1 5 10 15
97 ctg ccc aat cca gcc cat tcc agg ttc aat ccc atc cgc ctc ccc acc 96
98 Leu Pro Asn Pro Ala His Ser Arg Phe Asn Pro Ile Arg Leu Pro Thr
99 20 25 30
101 aca cac gaa ccc gcc 111
102 Thr His Glu Pro Ala
103 35

106 <210> SEQ ID NO: 4
107 <211> LENGTH: 37
108 <212> TYPE: PRT
109 <213> ORGANISM: Artificial Sequence
110 <220> FEATURE: insert
110 <223> OTHER INFORMATION: Description of Artificial Sequence: Signal peptide give source
112 <400> SEQUENCE: 4
113 Met Lys Ala Phe Thr Leu Ala Leu Phe Leu Ala Leu Ser Leu Tyr Leu
114 1 5 10 15
116 Leu Pro Asn Pro Ala His Ser Arg Phe Asn Pro Ile Arg Leu Pro Thr
117 20 25 30
119 Thr His Glu Pro Ala
120 35
124 <210> SEQ ID NO: 5
125 <211> LENGTH: 66
126 <212> TYPE: DNA
127 <213> ORGANISM: Artificial Sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Description of Artificial Sequence: Signal peptide
132 <220> FEATURE:
133 <221> NAME/KEY: sig_peptide

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/284,697
 DATE: 12/01/2000
 TIME: 08:23:23

Input Set : A:\ES.txt
 Output Set: N:\CRF3\12012000\I284697.raw

134 <222> LOCATION: (1)..(66)
 135 <223> OTHER INFORMATION: Signal peptide of rabbit gastric lipase
 137 <220> FEATURE:
 138 <221> NAME/KEY: CDS
 139 <222> LOCATION: (1)..(66)
 141 <400> SEQUENCE: 5
 142 atg tgg gtg ctt ttc atg gtg gca gct ttg cta tct gca ctt gga act 48
 143 Met Trp Val Leu Phe Met Val Ala Ala Leu Leu Ser Ala Leu Gly Thr
 144 1 5 10 15 66
 146 aca cat ggt ctt ttt gga
 147 Thr His Gly Leu Phe Gly
 148 20
 151 <210> SEQ ID NO: 6
 152 <211> LENGTH: 22
 153 <212> TYPE: PRT
 154 <213> ORGANISM: Artificial Sequence
 W--> 155 <220> FEATURE: *insert*
 155 <223> OTHER INFORMATION: Description of Artificial Sequence Signal peptide
 157 <400> SEQUENCE: 6
 158 Met Trp Val Leu Phe Met Val Ala Ala Leu Leu Ser Ala Leu Gly Thr
 159 1 5 10 15
 161 Thr His Gly Leu Phe Gly
 162 20
 166 <210> SEQ ID NO: 7
 167 <211> LENGTH: 48
 168 <212> TYPE: DNA
 169 <213> ORGANISM: Artificial Sequence
 171 <220> FEATURE:
 172 <223> OTHER INFORMATION: Description of Artificial Sequence Signal peptide
 174 <220> FEATURE:
 175 <221> NAME/KEY: sig_peptide
 176 <222> LOCATION: (1)..(48)
 177 <223> OTHER INFORMATION: Signal peptide of PSPHPL.
 179 <220> FEATURE:
 180 <221> NAME/KEY: CDS
 181 <222> LOCATION: (1)..(48)
 182 <223> OTHER INFORMATION: The cleavage sequence between the two sequences
 183 coding for PSPHPL and HPL is Gly-Lys.
 185 <400> SEQUENCE: 7
 186 atg ctg cca ctt Lgg act ctt tca ctg ctg ctg gga gca gta gca gga 48
 187 Met Leu Pro Leu Trp Thr Leu Ser Leu Leu Leu Gly Ala Val Ala Gly
 188 1 5 10 15
 191 <210> SEQ ID NO: 8
 192 <211> LENGTH: 16
 193 <212> TYPE: PRT
 194 <213> ORGANISM: Artificial Sequence
 W--> 195 <220> FEATURE: *insert*
 195 <223> OTHER INFORMATION: Description of Artificial Sequence Signal peptide
 197 <400> SEQUENCE: 8

do you mean rabbit?
give source
nucleotide sequence
give source

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/284,697

DATE: 12/01/2000

TIME: 08:23:23

Input Set : A:\ES.txt

Output Set: N:\CRF3\12012000\I284697.raw

198 Met Leu Pro Leu Trp Thr Leu Ser Leu Leu Gly Ala Val Ala Gly
 199 1 5 10 15

203 <210> SEQ ID NO: 9

204 <211> LENGTH: 66

205 <212> TYPE: DNA

206 <213> ORGANISM: Artificial Sequence

208 <220> FEATURE:

209 <223> OTHER INFORMATION: Description of Artificial Sequence: Signal peptide

211 <220> FEATURE:

212 <221> NAME/KEY: sig_peptide

213 <222> LOCATION: (1)..(66)

214 <223> OTHER INFORMATION: Signal peptide of HPCOL

216 <220> FEATURE:

217 <221> NAME/KEY: CDS

218 <222> LOCATION: (1)..(66)

220 <400> SEQUENCE: 9

221 atg tgg gtc ctt ttc atg gtc gca gct ttg cta tct gca ctt gga act 48

222 Met Trp Val Leu Phe Met Val Ala Ala Leu Leu Ser Ala Leu Gly Thr

223 1 5 10 15

225 aca cat ggt ctt ttt gga 66

226 Thr His Gly Leu Phe Gly

227 20

230 <210> SEQ ID NO: 10

231 <211> LENGTH: 22

232 <212> TYPE: PRT

233 <213> ORGANISM: Artificial Sequence

W---> 234 <220> FEATURE:

234 <223> OTHER INFORMATION: Description of Artificial Sequence: Signal peptide

236 <400> SEQUENCE: 10

237 Met Trp Val Leu Phe Met Val Ala Ala Leu Leu Ser Ala Leu Gly Thr

238 1 5 10 15

240 Thr His Gly Leu Phe Gly

241 20

245 <210> SEQ ID NO: 11

246 <211> LENGTH: 51

247 <212> TYPE: DNA

248 <213> ORGANISM: Artificial Sequence

250 <220> FEATURE:

251 <223> OTHER INFORMATION: Description of Artificial Sequence: Signal peptide

253 <220> FEATURE:

254 <221> NAME/KEY: sig_peptide

255 <222> LOCATION: (1)..(51)

256 <223> OTHER INFORMATION: Signal peptide of PSHPOL.

258 <220> FEATURE:

259 <221> NAME/KEY: CDS

260 <222> LOCATION: (1)..(51)

261 <223> OTHER INFORMATION: The cleavage sequence between the two sequences

262 coding for PSHPOL and HPCOL is Ala-Lys.

264 <400> SEQUENCE: 11

*nucleotide sequence**insert**gene source**nucleotide sequence*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/284,697

DATE: 12/01/2000

TIME: 08:23:23

Input Set : A:\ES.txt

Output Set: N:\CRF3\12012000\I284697.raw

RECEIVED

DEC 14 2000

TECH CENTER 1600/2900

265 atg gag aag atc ctg atc ctc ctg ctt gtc gcc ctc tct gtg gcc tat 48
 266 Met Glu Lys Ile Leu Ile Leu Leu Val Ala Leu Ser Val Ala Tyr
 267 1 5 10 15
 269 gca 51
 270 Ala
 273 <210> SEQ ID NO: 12
 274 <211> LENGTH: 17
 275 <212> TYPE: PRT
 276 <213> ORGANISM: Artificial Sequence
 W--> 277 <220> FEATURE: *insert*
 277 <223> OTHER INFORMATION: Description of Artificial Sequence *Signal peptide*
 279 <400> SEQUENCE: 12
 280 Met Glu Lys Ile Leu Ile Leu Leu Val Ala Leu Ser Val Ala Tyr
 281 1 5 10 15
 283 Ala
 288 <210> SEQ ID NO: 13
 289 <211> LENGTH: 32
 290 <212> TYPE: DNA
 291 <213> ORGANISM: Artificial Sequence
 293 <220> FEATURE:
 294 <223> OTHER INFORMATION: Description of Artificial
 295 Sequence: oligodeoxynucleotide
 297 <220> FEATURE:
 298 <221> NAME/KEY: misc_feature
 299 <222> LOCATION: (1)..(32)
 300 <223> OTHER INFORMATION: Oligodeoxynucleotide used to construct the adapter
 301 carrying restriction sites PacI, AscI, MluI and
 302 HpaI.
 304 <400> SEQUENCE: 13
 305 agotgattaa ttaagggcgcg ccacgcgtta ac 32
 308 <210> SEQ ID NO: 14
 309 <211> LENGTH: 32
 310 <212> TYPE: DNA
 311 <213> ORGANISM: Artificial Sequence
 313 <220> FEATURE:
 314 <223> OTHER INFORMATION: Description of Artificial
 315 Sequence: oligodeoxynucleotide
 317 <220> FEATURE:
 318 <221> NAME/KEY: misc_feature
 319 <222> LOCATION: (1)..(32)
 320 <223> OTHER INFORMATION: Oligodeoxynucleotide used to construct the adapter
 321 carrying the restriction sites PacI, AscI, MluI
 322 and HpaI.
 324 <400> SEQUENCE: 14
 325 aattgttaac gcgaggcgcg cottaattaa tc 32
 328 <210> SEQ ID NO: 15
 329 <211> LENGTH: 523
 330 <212> TYPE: DNA
 331 <213> ORGANISM: Homo sapiens

give name

VERIFICATION SUMMARY

DATE: 12/01/2000

PATENT APPLICATION: US/09/284,697

TIME: 08:23:24

Input Set : A:\ES.txt

Output Set: N:\CRF3\12012000\I284697.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:42 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-DD,MMM-YYYY or Season-YYYY
L:58 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:90 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-DD,MMM-YYYY or Season-YYYY
L:110 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:155 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:195 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:234 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:277 M:258 W: Mandatory Feature missing, <220> FEATURE: